\_\_\_\_\_\_

Sequence Listing could not be accepted due to errors.

See attached Validation Report.

If you need help call the Patent Electronic Business Center at (866) 217-9197 (toll free).

Reviewer: Anne Corrigan

Timestamp: [year=2010; month=7; day=27; hr=11; min=15; sec=3; ms=141; ]

\_\_\_\_\_\_

\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*

Reviewer Comments:

<400> 13

ggaggagat atg cag ttt gca ctt gca ttg gac acg aac tca ggt cct cac 51

Met Gln Phe Ala Leu Ala Leu Asp Thr Asn Ser Gly Pro His

1 5 10

- cag ata aga tct tgt gag ggt gat ggg att gac agg ttg gaa aaa tta 99
  Gln Ile Arg Ser Cys Glu Gly Asp Gly Ile Asp Arg Leu Glu Lys Leu
  15 20 25 30
- agt att ggg ggc aga aag cag gag aaa gct ttg aga aat agg tgc ttt 147
  Ser Ile Gly Gly Arg Lys Gln Glu Lys Ala Leu Arg Asn Arg Cys Phe

  35
  40
  45
- ggt ggt aga gtt gct gca act aca caa tgt att ctt acc tca gat gct 195

  Gly Gly Arg Val Ala Ala Thr Thr Gln Cys Ile Leu Thr Ser Asp Ala

  50 55 60
- tgt cct gaa act ctt cat tct caa aca cag tcc tct agg aaa aat tat 243

  Cys Pro Glu Thr Leu His Ser Gln Thr Gln Ser Ser Arg Lys Asn Tyr

  65 70 75
- gct gat gca aac cgt gta tct gck atc att ttg ggc gga ggc act gga 291
- Ala Asp Ala Asn Arg Val Ser Ala Ile Ile Leu Gly Gly Gly Thr Gly 80 85 90

Please remove the blank line between the above row of codons and their respective amino acids; the amino acids should appear directly below their their codons.

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<210> 15
<211> 1576
<212> DNA
<213> Zea mays
<220>
<221> CDS
<222> (10)..(1563)
<223> Shrunken-2 gene revertant form, modified to be
      heat stable
<220>
<221> variation
<222> (267)
\langle 223 \rangle k = g or t; amino acid 86 = Ala.
<220>
<221> variation
<222> (1008)
<223> y = c or t.
<220>
<221> variation
<222> (1368)
\langle 223 \rangle r = a or g; amino acid 453 = Pro.
<220>
<221> variation
<222> (1578)
<223> k = g or t.
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ggaggagat atg cag ttt gca ctt gca ttg gac acg aac tca ggt cct cac 51
          Met Gln Phe Ala Leu Ala Leu Asp Thr Asn Ser Gly Pro His
             1
                              5
                                                   10
cag ata aga tct tgt gag ggt gat ggg att gac agg ttg gaa aaa tta
                                                                        99
Gln Ile Arg Ser Cys Glu Gly Asp Gly Ile Asp Arg Leu Glu Lys Leu
 15
                      20
                                            25
                                                                  30
```

agt att ggg ggc aga aag cag gag aaa gct ttg aga aat agg tgc ttt

ser	тте	СΤΆ	СΤΆ	35	туѕ	GTII	Glu	туѕ	40	Leu	Arg	ASII	Arg	45	rne	
ggt	ggt	aga	gtt	gct	gca	act	aca	caa	tgt	att	ctt	acc	tca	gat	gct	195
Gly	Gly	Arg	Val	Ala	Ala	Thr	Thr	Gln	Cys	Ile	Leu	Thr	Ser	Asp	Ala	
			50					55					60			
_		_					caa		_							243
Cys	Pro	GLu 65	Thr	Leu	His	Ser	Gln 70	Thr	Gln	Ser	Ser	Arg 75	Lys	Asn	Tyr	
gct	gat	gca	aac	cgt	gta	tct	gck	atc	att	ttg	ggc	gga	ggc	act	gga	291
Ala	_	Ala	Asn	Arg	Val		Ala	Ile	Ile	Leu	_	Gly	Gly	Thr	Gly	
	80					85					90					
	_				_		agc		_	_	_					339
	Gln	Leu	Phe	Pro	Leu 100	Thr	Ser	Thr	Arg		Thr	Pro	Ala	Val		
95					100					105					110	
_			_				att	_			_	_		_		387
Val	Gly	Gly	Cys	Tyr 115	Arg	Leu	Ile	Asp	11e 120	Pro	Met	Ser	Asn	Cys 125	Phe	
	_				_		ttt -:		_	_	_					435
Asn	Ser	Gly	11e 130	Asn	Lys	Ile	Phe	Val 135	Met	Ser	GIn	Phe	140	Ser	Thr	
tcg	ctt	aac	cgc	cat	att	cat	cgt	aca	tac	ctt	gaa	ggc	ggg	atc	aac	483
Ser	Leu	Asn 145	Arg	His	Ile	His	Arg 150	Thr	Tyr	Leu	Glu	Gly 155	Gly	Ile	Asn	
ttt	gct	gat	gga	tct	gta	cag	gta	tta	gcg	gct	aca	caa	atg	cct	gaa	531
Phe		Asp	Gly	Ser	Val		Val	Leu	Ala	Ala		Gln	Met	Pro	Glu	
	160					165					170					
		_				_	ggt			_			_			579
	Pro	Ala	Gly	Trp		Gln	Gly	Thr	Ala	_	Ser	Ile	Arg	Lys		
175					180					185					190	
atc	tgg	gta	ctc	gag	gat	tat	tac	agt	cac	aaa	tcc	att	gac	aac	att	627
Ile	Trp	Val	Leu	Glu	Asp	Tyr	Tyr	Ser	His	Lys	Ser	Ile	Asp	Asn	Ile	

gta	atc	ttg	agt	ggc	gat	cag	ctt	tat	cgg	atg	aat	tac	atg	gaa	ctt	675
Val	Ile	Leu	Ser	Gly	Asp	Gln	Leu	Tyr	Arg	Met	Asn	Tyr	Met	Glu	Leu	
			210					215					220			
at a	Cac	222	cat	at a	asa	gac	ca+	act	ast.	a+ c	act	a+ a	+ < >	+ ~+	act	723
	_			_		_	_	_	_					_	_	125
vai	GIII	_	HIS	vai	GIU	Asp	_	Ата	Asp	тте	Inr		ser	Cys	Ala	
		225					230					235				
cct	gtt	gat	gag	agc	cga	gct	tct	aaa	aat	aaa	cta	gtg	aag	att	gat	771
Pro	Val	Asp	Glu	Ser	Arg	Ala	Ser	Lys	Asn	Gly	Leu	Val	Lys	Ile	Asp	
	240					245					250					
cat	act	gga	cgt	gta	ctt	caa	ttc	ttt	gaa	aaa	сса	aag	ggt	gct	gat	819
						Gln										
255		- 1	ر		260					265		<u> </u>	- 1		270	
200					200					200					2,0	
++ ~	t	+ ~+	a + a	~ ~ ~	~++	~~~~	222	222	++~	a+ a	200	+ - +	~a+	a+ a	or a t	067
_			_	_	_	gag				_	_		_		_	867
Leu	Asn	Ser	Met	_	val	Glu	Thr	Asn		Leu	Ser	Tyr	Ala		Asp	
				275					280					285		
gat	gca	cag	aaa	tat	сса	tac	ctt	gca	tca	atg	ggc	att	tat	gtc	ttc	915
Asp	Ala	Gln	Lys	Tyr	Pro	Tyr	Leu	Ala	Ser	Met	Gly	Ile	Tyr	Val	Phe	
			290					295					300			
aaq	aaa	gat	qca	ctt	tta	gac	ctt	ctc	aaq	tca	aaa	tat	act	caa	tta	963
_		_	_			Asp			_							
_1 ~	_1 ~	305					310		-10	001	-10	315		0		
		303					510					515				
~~+			0.0.0	+ ~+		o + o	~+~	~~~		~ ~ <del>+</del>	ort o	~+ ~	~~+	+	o ort-	1 \ 1 1
	_				_	atc			_	_	_		_	_	_	1011
Hls	_	Phe	GLy	Ser	Glu	Ile	Leu	Pro	Arg	Ala		Leu	Asp	Tyr	Ser	
	320					325					330					
gtg	cag	gca	tgc	att	ttt	acg	ggc	tat	tgg	gag	gat	gtt	gga	aca	atc	1059
Val	Gln	Ala	Cys	Ile	Phe	Thr	Gly	Tyr	Trp	Glu	Asp	Val	Gly	Thr	Ile	
335					340					345					350	
aaa	tca	ttc	ttt	gat	qca	aac	tta	acc	ctc	act	gag	caa	cct	tcc	aaq	1107
						Asn										
y D		1 110	1 110	355	111 U	11011	пси	111 U	360		O T U	0 1 11	110	365	٠,٧	
				223					200					203		

	_			_	cca Pro							_		_	_	1155
_		_	_		ttg Leu	_	_	_	_	_			_			1203
					ctg Leu											1251
					gtc Val 420											1299
_	_				atc Ile		_		_	_	_	_		_		1347
					gtc Val											1395
		_			gac Asp	_	Asn	Ala			Gly	_				1443
					ggc Gly											1491
					gga Gly 500					_	_		_			1539
	gat Asp			_	ata Ile	taga	atcg	gct (	gcgt}	ktgc	9					1576

1) Please remove the blank line between the above row of codons and their amino acids; 2) the above <220>-<223> section describing "k" at

```
Same errors in Sequences 17, 19, 21, 23, 25, 27, 29, 31, 35, 37, 39 and
41.
<210> 33
<211> 1576
<212> DNA
<213> Zea mays
<220>
<221> CDS
<222> (10)..(1563)
<223> Shrunken-2 gene revertant form, modified to be
      heat stable
<220>
<221> variation
<222> (267)
\langle 223 \rangle k = g or t; amino acid 86 = Ala.
<220>
<221> variation
<222> (1008)
<223> y = c or t.
<220>
<221> variation
<222> (1368)
\langle 223 \rangle r = a or g; amino acid 453 = Pro.
<220>
<221> variation
<222> (1578)
<223> k = q or t.
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ggaggagat atg cag ttt gca ctt gca ttg gac acg aac tca ggt cct cac 51
          Met Gln Phe Ala Leu Ala Leu Asp Thr Asn Ser Gly Pro His
                              5
             1
                                                   10
```

location 1578 is incorrect; the sequence only has 1576 nucleotides.

cag ata aga tot tgt gag ggt gat ggg att gac agg ttg gaa aaa tta 99 Gln Ile Arg Ser Cys Glu Gly Asp Gly Ile Asp Arg Leu Glu Lys Leu

			ggc Gly										147
		_	gtt Val 50	_	_		_				_	_	195
_		_	act Thr				_						243
			aac Asn										291
	_		ttt Phe		_	_	_	_	_	_	_		339
			tgt Cys										387
	_		ata Ile 130		_		 _	_	_				435
_			cgc Arg			_			_	 			483
			gga Gly										531
			gga Gly										579

atc	tgg	gta	ctc	gag	gat	tat	tac	agt	cac	aaa	tcc	att	gac	aac	att	627
Ile	Trp	Val	Leu	Glu	Asp	Tyr	Tyr	Ser	His	Lys	Ser	Ile	Asp	Asn	Ile	
				195					200					205		
gta	atc	ttg	agt	ggc	gat	cag	ctt	tat	cgg	atg	aat	tac	atg	gaa	ctt	675
Val	Ile	Leu	Ser	Gly	Asp	Gln	Leu	Tyr	Arg	Met	Asn	Tyr	Met	Glu	Leu	
			210	_	_			215	_			_	220			
gtg	caq	aaa	cat	gtc	gag	gac	gat	gct	gat	atc	act	ata	tca	tgt	gct	723
					Glu											
		225				_	230		_			235		_		
cct	gtt	gat	qaq	agc	cga	gct	tct	aaa	aat	aaa	cta	ata	aaq	att	gat	771
	_	-		_	Arg	-							_		_	
	240	_				245		_		_	250				-	
cat	act	gga	cat	qta	ctt	caa	ttc	ttt	gaa	aaa	сса	aaq	aat	act	gat	819
			_	_	Leu				-			_		-	_	
255		1			260					265					270	
					_ , ,					_ , ,					_ , ,	
t.t.a	aat.	tct	at.q	aσa	gtt	aaa	acc	aac	ttc	cta	agc	tat	act.	ata	gat.	867
					Val											
				275					280			-1-		285	1	
aat.	aca	caq	aaa	t.at.	сса	tac	ct.t.	aca	t.ca	at.a	aac	at.t.	t.at.	at.c	t.t.c	915
_	_	_			Pro			_		_				_		
			290	-1-		-1-		295			1		300			
aaσ	aaa	αat.	gca	ct.t.	tta	gac	ct.t.	ct.c	aaσ	t.ca	aaa	t.at.	act.	caa	t.t.a	963
					Leu											
-1-	-1-	305				1	310		-1-		-1-	315				
cat.	gac	t.t.t.	aaa	t.ct.	gaa	at.c	ct.c	cca	aga	act.	at.a	ct.a	αat.	at.a	agt.	1011
	_				Glu				_	-	-		-	_	_	
	320				0 = 0.	325			5		330	_ 0 0.				
	020					020										
ata	cad	aca	tac	att	ttt	aca	aac	tat	t.aa	aaa	gat	at t	aaa	aca	atc	1059
	_	_	_		Phe	_					_	_				
335	U - 11		~ <u>,</u>		340		~ ± <u>y</u>	- 1 -		345			∪ ± <u>y</u>		350	
					0 1 0					0 10						
aaa	t.ca	t.t c	+.++	gat	gca	aac	t.t a	acc	ctc	act	gag	cad	cat	t.cc	aaq	1107
					Ala											110,
-72	$\sim$ $\sim$ $\perp$		_ 11	- 10 P	4 3 T U	41011	u	4 3 T U	_ u		$\circ$ $\perp$ $\alpha$	$\sim$ $\pm$ 11	0	$\sim$ $\sim$ $\perp$	-y U	

ttt	gat	ttt	tac	gat	сса	aaa	aca	cct	ttc	ttc	act	gca	CCC	cga	tgc	1155
Phe	Asp	Phe	Tyr	Asp	Pro	Lys	Thr	Pro	Phe	Phe	Thr	Ala	Pro	Arg	Cys	
			370					375					380			
ttg	cct	ccg	acg	caa	ttg	gac	aag	tgc	aag	atg	aaa	tat	gca	ttt	atc	1203
Leu	Pro	Pro	Thr	Gln	Leu	Asp	_	Cys	Lys	Met	Lys	_	Ala	Phe	Ile	
		385					390					395				
<b>.</b>			4					<b>.</b>								1051
	_	ggt	_		_	_	_	_								1251
ser	400	Gly	Cys	ьеи	ьеи	405	GIU	Cys	ASII	тте	410	птѕ	ser	Val	тте	
	400					400					410					
aaa	atc	tgc	tca	cat	atc	agc	tct	aaa	tat	gaa	ctc	aaq	gac	tcc	ata	1299
		Cys														
415		_			420			_	_	425		_	_		430	
atg	atg	gga	gcg	gac	atc	tat	gaa	act	gaa	gaa	gaa	gct	tca	aag	cta	1347
Met	Met	Gly	Ala	Asp	Ile	Tyr	Glu	Thr	Glu	Glu	Glu	Ala	Ser	Lys	Leu	
				435					440					445		
ctg	tta	gct	aaa	aag	gtc	ccr	gtt	gga	ata	gga	agg	aac	aca	aag	ata	1395
Leu	Leu	Ala	_	Lys	Val	Pro	Val	_	Ile	Gly	Arg	Asn	Thr	Lys	Ile	
			450					455					460			
		tgt			_	_		_				_				1443
Arg	Asn	Cys	lle	lle	Asp	Met		Ala	Arg	lle	GLY	_	Asn	Val	Val	
		465					470					475				
atc	202	aac	act	220	aac	atc	Caa	asa	act	cat	Cac	cca	cra a	C a a	aaa	1491
		Asn														1491
110	480	11011	001	<b>L</b> 10	CTY	485	0111	OIU	1114	110P	490	110	OIG	OIU	O±1	
tac	tac	ata	agg	tct	gga	atc	gtg	gtg	atc	ctg	aag	aat	gca	acc	atc	1539
		Ile														
495	_		_		500					505	_				510	
aac	gat	aaa	tct	gtc	ata	taga	atcg	gct q	gcgtl	ctgc	3					1576
Asn	Asp	Gly	Ser	Val	Ile											

Two errors above: 1) the <220>-<223> section describing the "y" at location 1008 is errored: "g" is at locadtion 1008; 2) the <220>-<223> section describing the "k" at location 1578 is errored: there are only 1576 nucleotides above.

\*\*\*\*\*\*\*\*\*\*\*\*

## Validated By CRFValidator v 1.0.3

Application No: 10569000 Version No: 2.0

Input Set:

Output Set:

**Started:** 2010-07-22 16:44:17.022

Finished: 2010-07-22 16:44:19.919

**Elapsed:** 0 hr(s) 0 min(s) 2 sec(s) 897 ms

Total Warnings: 0

Total Errors: 112

No. of SeqIDs Defined: 42

Actual SeqID Count: 42

Err	or code	Error Descr	ption						
E	336	Empty lir	es foun	d between	the	proteins	and	the	dna
E	336	Empty lir	es foun	d between	the	proteins	and	the	dna
E	336	Empty lin	es foun	d between	the	proteins	and	the	dna
E	336	Empty lir	es foun	d between	the	proteins	and	the	dna
E	336	Empty lir	es foun	d between	the	proteins	and	the	dna
E	336	Empty lir	es foun	d between	the	proteins	and	the	dna
E	336	Empty lir	es foun	d between	the	proteins	and	the	dna
E	336	Empty lir	es foun	d between	the	proteins	and	the	dna
Ε	336	Empty lir	es foun	d between	the	proteins	and	the	dna
Ε	336	Empty lir	es foun	d between	the	proteins	and	the	dna
Ε	336	Empty lir	es foun	d between	the	proteins	and	the	dna
E	336	Empty lir	es foun	d between	the	proteins	and	the	dna
E	336	Empty lir	es foun	d between	the	proteins	and	the	dna
Ε	336	Empty lir	es foun	d between	the	proteins	and	the	dna
Ε	336	Empty lir	es foun	d between	the	proteins	and	the	dna
E	336	Empty lir	es foun	d between	the	proteins	and	the	dna
E	336	Empty lir	es foun	d between	the	proteins	and	the	dna
Ε	336	Empty lir	es foun	d between	the	proteins	and	the	dna
Ε	336	Empty lir	es foun	d between	the	proteins	and	the	dna
E	336	Empty lin	es foun	d between	the	proteins	and	the	dna

Input Set:

Output Set:

**Started:** 2010-07-22 16:44:17.022 **Finished:** 2010-07-22 16:44:19.919

**Elapsed:** 0 hr(s) 0 min(s) 2 sec(s) 897 ms

Total Warnings: 0
Total Errors: 112

No. of SeqIDs Defined: 42

Actual SeqID Count: 42

Error code Error Description

This error has occured more than 20 times, will not be displayed

## SEQUENCE LISTING

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<110> University of Florida Research Foundation, Inc.
      Hannah, L. Curtis
      Lyerly Linebarger, Carla R.
<120> Heat Stable Variants of Adenosine Diphosphate Glucose Pyrophosphorylase
<130> UF-371XC1 PCT
<140> 10569000
<141> 2010-07-22
<150> US 60/496,188
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                                                                   120
gctcatgata gtgttcttgg aatcattctg ggaggtggtg ctgggactag attgtacccc
                                                                    180
ttgacaaaga agcgtgccaa gcctgcagtg ccattgggtg ccaactatag actgattgat
                                                                     240
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                                                                     300
aactctgctt ccctcaaccg tcacctctca agagcctacg ggagcaacat tggagggtac
                                                                     360
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                                                                     420
tttcagggta ctgcagatgc tgtaaggcag tacttgtggt tgtttgagga gcataatgtg
                                                                     480
                                                                     540
atggaatttc taattcttgc tggcgatcac ctgtaccgga tggactatga aaagttcatt
caggcacaca gagaaacaaa tgctgatatt accgttgctg ccctaccgat ggatgagaaa
                                                                     600
cgtgcaactg catttggcct catgaaaatt gatgaagaag ggaggatcat tgagtttgct
                                                                     660
                                                                     720
gagaaaccga aaggagagca gttgaaagca atgatggttg acaccaccat acttggcctt
gatgacgtga gggcaaagga aatgccttat attgctagca tgggtatcta tgttttcagc
                                                                     780
aaagatgtaa tgcttcagct cctccgtgaa caatttcctg aagccaatga ctttggaagt
                                                                     840
                                                                     900
gaggttattc caggtgcaac cagcattgga aagagggttc aggcttatct gtatgatggt
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tactgggaag atatcggtac cattgcggca ttttataatg caaacttggg aataaccaag

aagccaatac	cagatttcag	cttctatgac	cgttttgctc	caatttatac	acaacctcga	1020
cacctgccac	cttcaaaggt	tcttgatgct	gatgtgacag	acagtgttat	tggtgaagga	1080
tgtgttatta	aaaactgcaa	gataaaccat	tctgtagttg	gactccgatc	ttgcatatct	1140
gaaggtgcta	tcatagagga	cagtttacta	atgggtgcgg	actactatga	gacagaagct	1200
gataaaaaac	tccttgccga	aaaaggtggc	attcctattg	gtattgggaa	aaattcatgc	1260
atcaggagag	caatcattga	caagaatgct	cgaattggag	acaatgttaa	gatactcaat	1320
gctgacaatg	ttcaagaagc	tgcaatggag	acagacgggt	acttcatcaa	aggtggaatt	1380
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<211> 475

<212> PRT

<213> zea mays

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Thr Ala Ala Glu Gln Pro Ile Pro Lys Arg Asp Lys Ala Ala Asn 20 25 30

Asp Ser Thr Tyr Leu Asn Pro Gln Ala His Asp Ser Val Leu Gly Ile 35 40 45

Ile Leu Gly Gly Gly Ala Gly Thr Arg Leu Tyr Pro Leu Thr Lys Lys
50 55 60

Arg Ala Lys Pro Ala Val Pro Leu Gly Ala Asn Tyr Arg Leu Ile Asp 65 70 75 80

Ile Pro Val Ser Asn Cys Leu Asn Ser Asn Ile Ser Lys Ile Tyr Val
85 90 95

Leu Thr Gln Phe Asn Ser Ala Ser Leu Asn Arg His Leu Ser Arg Ala 100 105 110

Tyr Gly Ser Asn Ile Gly Gly Tyr Lys Asn Glu Gly Phe Val Glu Val 115 120 125

Leu Ala Ala Gln Gln Ser Pro Asp Asn Pro Asn Trp Phe Gln Gly Thr 130 135 140

Met Glu Phe Leu Ile Leu Ala Gly Asp His Leu Tyr Arg Met Asp Tyr

165 170 17

Glu	Lys	Phe	Ile	Gln	Ala	His	Arg	Glu	Thr	Asn	Ala	Asp	Ile	Thr	Val
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Ala	Ala	Leu 195	Pro	Met	Asp	Glu	Lys 200	Arg	Ala	Thr	Ala	Phe 205	Gly	Leu	Met
Lys	Ile 210	Asp	Glu	Glu	Gly	Arg 215	Ile	Ile	Glu	Phe	Ala 220	Glu	Lys	Pro	Lys
Gly 225	Glu	Gln	Leu	Lys	Ala 230	Met	Met	Val	Asp	Thr 235	Thr	Ile	Leu	Gly	Leu 240
Asp	Asp	Val	Arg	Ala 245	Lys	Glu	Met	Pro	Tyr 250	Ile	Ala	Ser	Met	Gly 255	Ile
Tyr	Val	Phe	Ser 260	Lys	Asp	Val	Met	Leu 265	Gln	Leu	Leu	Arg	Glu 270	Gln	Phe
Pro	Glu	Ala 275	Asn	Asp	Phe	Gly	Ser 280	Glu	Val	Ile	Pro	Gly 285	Ala	Thr	Ser
Ile	Gly 290	Lys	Arg	Val	Gln	Ala 295	Tyr	Leu	Tyr	Asp	Gly 300	Tyr	Trp	Glu	Asp
Ile 305	Gly	Thr	Ile	Ala	Ala 310	Phe	Tyr	Asn	Ala	Asn 315	Leu	Gly	Ile	Thr	Lys 320
Lys	Pro	Ile	Pro	Asp 325	Phe	Ser	Phe	Tyr	Asp 330	Arg	Phe	Ala	Pro	Ile 335	Tyr
Thr	Gln	Pro	Arg 340	His	Leu	Pro	Pro	Ser 345	Lys	Val	Leu	Asp	Ala 350	Asp	Val
Thr	Asp	Ser 355	Val	Ile	Gly	Glu	Gly 360	Cys	Val	Ile	Lys	Asn 365	Суз	Lys	Ile
Asn	His 370	Ser	Val	Val	Gly	Leu 375	Arg	Ser	Суз	Ile	Ser 380	Glu	Gly	Ala	Ile
Ile 385	Glu	Asp	Ser	Leu	Leu 390	Met	Gly	Ala	Asp	Tyr 395	Tyr	Glu	Thr	Glu	Ala 400
Asp	Lys	Lys	Leu	Leu 405	Ala	Glu	Lys	Gly	Gly 410	Ile	Pro	Ile	Gly	Ile 415	Gly
Lys	Asn	Ser	Cys 420	Ile	Arg	Arg	Ala	Ile 425	Ile	Asp	Lys	Asn	Ala 430	Arg	Ile
Gly	Asp	Asn 435	Val	Lys	Ile	Leu	Asn 440	Ala	Asp	Asn	Val	Gln 445	Glu	Ala	Ala
Met	Glu 450	Thr	Asp	Gly	Tyr	Phe 455	Ile	Lys	Gly	Gly	Ile 460	Val	Thr	Val	Ile
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245 250 255

Tyr Val Phe	Ser Lys 260	Asp Val	Met Leu 265		eu Leu	Arg Gl		Phe
Pro Glu Ala 275	Asn Asp	Phe Gly	Ser Glu 280	ı Val I	le Pro	Gly Al	a Thr	Ser
Ile Gly Lys 290	Arg Val	Gln Ala 295	Tyr Lei	ı Tyr A	sp Gly 300	Tyr Tr	o Glu	Asp
Ile Gly Thr	Ile Ala	Ala Phe 310	Tyr Asr		sn Leu 15	Gly Il	e Thr	Lys 320
Lys Pro Ile	Pro Asp 325	Phe Ser	Phe Tyı	330	rg Phe	Ala Pr	335	Tyr
Thr Gln Pro	Arg His	Leu Pro	Pro Ser	_	al Leu	Asp Al	-	Val
Thr Asp Ser 355	Val Ile	Gly Glu	Gly Cys	: Val I	le Lys	Asn Cy 365	s Lys	Ile
Asn His Ser 370	Val Val	Gly Leu 375	Arg Sei	Cys I	le Ser 380	Glu Gl	y Ala	Ile
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Lys Asn Ser	Cys Ile	Arg Arg	Ala Ile		sp Lys	Asn Ala	_	Ile
Gly Asp Asn 435	Val Lys	Ile Leu	Asn Ala	a Asp A	sn Val	Gln Gl	u Ala	Ala
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Ile Ile Leu Gly Gly Gly Ala Gly Thr Arg Leu Tyr Pro Leu Thr Lys Lys Arg Ala Lys Pro Ala Val Pro Leu Gly Ala Asn Tyr Arg Leu Ile Asp Ile Pro Val Ser Asn Cys Leu Asn Ser Asn Ile Ser Lys Ile Tyr Val Leu Thr Gln Phe Asn Ser Ala Ser Leu Asn Arg His Leu Ser Arg Ala Tyr Gly Ser Asn Ile Gly Gly Tyr Lys Asn Glu Gly Phe Val Glu Val Leu Ala Ala Gln Gln Ser Pro Asp Asn Pro Asn Trp Phe Gln Gly Thr Ala Asp Ala Val Arg Gln Tyr Leu Trp Leu Phe Glu Glu His Asn Val Met Glu Phe Leu Ile Leu Ala Gly Asp His Leu Tyr Arg Met Asp Tyr Glu Lys Phe Ile Gln Ala His Arg Glu Thr Asn Ala Asp Ile Thr Val Ala Ala Leu Pro Met Asp Glu Lys Arg Ala Thr Ala Phe Gly Leu Met Lys Ile Asp Glu Glu Gly Arg Ile Ile Glu Phe Ala Glu Lys Pro Lys Gly Glu Gln Leu Lys Ala Met Met Val Asp Thr Thr Ile Leu Gly Leu Asp Asp Val Arg Ala Lys Glu Met Pro Tyr Ile Ala Ser Met Gly Ile Tyr Val Phe Ser Lys Asp Val Met Leu Gln Leu Leu Arg Glu Gln Phe Pro Glu Ala Asn Asp Phe Gly Ser Glu Val Ile Pro Gly Ala Thr 275 280 Ser Ile Gly Lys Arg Val Gln Ala Tyr Leu Tyr Asp Gly Tyr Trp Glu Asp Ile Gly Thr Ile Ala Ala Phe Tyr Asn Ala Asn Leu Gly Ile Thr Lys Lys Pro Ile Pro Asp Phe Ser Phe Tyr Asp Arg Phe Ala Pro Ile

Tyr Thr Gln Pro Arg His Leu Pro Pro Ser Lys Val Leu Asp Ala Asp

340 345 350

Val Thr Asp Ser Val Ile Gly Glu Gly Cys Val Ile Lys Asn Cys Lys 355 360 365

Ile Asn His Ser Val Val Gly Leu Arg Ser Cys Ile Ser Glu Gly Ala 370 375 380

Ile Ile Glu Asp Ser Leu Leu Met Gly Ala Asp Tyr Tyr Glu Thr Glu 385 390 395 400

Ala Asp Lys Lys Leu Leu Ala Glu Lys Gly Gly Ile Pro Ile Gly Ile 405 410 415

Gly Lys Asn Ser Cys Ile Arg Arg Ala Ile Ile Asp Lys Asn Ala Arg \$420\$